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1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuG1 17
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17 LeuLeuValValValValValValValValValValValVal 29
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112 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 161
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40 .....AspSerValCysProGlnGlyLysTyrTyr 39
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|||||
40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThr 56
|||||
212 CAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATA 261
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56 rLeuTyrAsnAspCysProGlnGlyLysTyrTyrTyrTyrTyr 73
|||||
262 CTCTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 311
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73 ysdLuSerGlySerPheThrAlaSerGlnAsnHisLeuArqHisCysLeu 89
|||||
312 GTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361
|||||
90 SerCysSerCysCysCysCysCysCysCysCysCysCysCysCys 406
|||||
362 AGCTGCTGCAAAATGGGAGAGAGAGAGAGAGAGAGAGAGAGAT 411
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106 sThrValAspArqAspThrValCysGlyCysArqLysAsnGlnTyrArq 123
|||||
412 CACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 461
|||||
123 IsTyrTrpSerGlnAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 139
|||||
462 ATTATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 511
|||||
140 AsnGlyThrValHisLeuSerCysGlnGlyLysGlnAsnThrValCys 156
|||||
512 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 561
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156 rCysHisAlaGlyPheLeuArqGlnAsnGlnCysValSerCysSerA 173
|||||
562 CTGCAATGCAAGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 611
|||||
173 sncysLysLysSerLeuGlnCysThrLysLeuCysLeuProGlnHis 189
|||||
612 ACTGTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 661
|||||
190 AsnValLysGlyThrGlnAspSerGlyThrThr 200
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662 AATGTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 694
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seq_name: qb_esl1:AL577008

seq_documentation_block:
LOCUS AL577008 675 bp mRNA
DEFINITION AL577008 IT1.NF1006.PL2 Homo sapiens cDNA clone CS001082YA01.5
Primer, mRNA sequence.
ACCESSION AL577008
VERSION AL577008.1 GI:12930716
KEYWORDS EST.

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human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates, Catarrhini, Hominidae; Homo. 1 (bases 1 to 975)

AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

location/Qualifiers

1. 975

organism="Homo sapiens"

db_xref="taxon:9606"

clone="CS001082YA01"

clone_lib="IT1.NF1006.PL2"

tissue_type="placenta"

note "Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI oligo(HT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies. Contact: Feng Liang life technologies, a division of invitrogen 9800 Medical Center drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifestech.com URL: http://lifestech.invitrogen.com

BASE COUNT 231 a 258 c 259 g 221 t 6 others

ORIGIN

alignment_scores:

Quality: 1074.50 Length: 211

Ratio: 5.482 Gaps: 2

Percent Similarity: 92.891 Percent Identity: 92.417

alignment_block:

US-09-525-998a-12 x AL577008

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17 LeuLeuValValValValValValValValValValValVal 29

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306 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 355

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30AspSerValCysProGlnGlyLysTyrTyr 39

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356 TATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 405

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40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThr 56

|||||

406 CAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATA 455

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56 rLeuTyrAsnAspCysProGlnGlyLysTyrTyrTyrTyrTyr 73

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|||||

506 GTGAGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 555

|||||

90 SerCysSerCysCysCysCysCysCysCysCysCysCysCysCys 106

|||||

556 AGCTGCTGCAAAATGGGAGAGAGAGAGAGAGAGAGAGAGAGAT 605

|||||

106 sThrValAspArqAspThrValCysGlyCysArqLysAsnGlnTyrArq 123

|||||

Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki
Y., Sugano, S., Isogai, T.)
Unpublished (2000)
JOURNAL
COMMENT
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yasa, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5' & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction, Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. 845
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NT2RM4"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/note="vector: pM18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"

FEATURES

SOURCE

BASE COUNT

ORIGIN

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Ratio: 5.188 Gaps: 2
Percent Similarity: 92.754 Percent Identity: 90.822

alignment_block:
us-09-525-998a-12 x A0124446

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220 AAGGCGGCTGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 269
17 dLeuLeuValIleTyProSerGlyValIleGly
|||||
270 GCGCTGCGCGCAATATGCTTACAGCGGCTGCTGCGCGCGCGCGCGCGCG 319
40 ASPSerValCysProGlnClyIleGly 39
|||||
420 TAGGATATG 369
40 HisProGlnAspAsnSerIleCysCysThrIleCysCysHisGlyIleThr 56
|||||
470 CAGCGCTCAAAATATTCGATTCCTGTAGCAAGTGCACAAAGGACCTTA 419
56 rLeuTyAspAspCysProGlyProGlyValIleAspThrAspCysAlaGluC 73
|||||
420 CTGTAACAAACACGTCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 469
73 ySGluSerGlySerPheIleAlaSerGluAsnHisLeuArqHisCysLeu 89
|||||
470 GTRAGAGAGCGCTGCTTCACGCGCTTCAGAAAGACGTCAGACACTGCGCTC 519
90 SerGlySerIleCysAlaPheGluMetClyGlnValGluIleSerSerCys 106
|||||
520 AGTGGCTCAAAATATTCGATTCCTGTAGCAAGTGCACAAAGGACCTTA 569
106 sThrValAspArqAspThrValCysGlyCysArqIleAsnIleTyArqH 123
|||||
570 CACAGTGAACCGGACACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 619
123 iSyrTrpSerGluAsnLeuPheGlnCysHisAsnCysSerLeuCysLeu 139
|||||
620 ATTATGAGTGAAGACCTTTTTCAGTGGTTCAATTGACAGCGCTGCGCTC 669

140 AssGlyThrValHisLeuSerCysGlnGluIleCysGluAsnThrValCysTh 156
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670 AATGGGACCTGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
156 rCysHisAlaGlyPheLeuArqGluAsnGluCysValSerCysSerA 173
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720 CTGCGATGCAAGTTCCTTCGAAAGAGAAAGCAATGCTGCTGCTGCTGCTA 768
173 sNCysIleTySerIleuGluCysThrIleCysLeuCysProGlnIleGlu 189
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769 ACTGTAAAGAAAGATCTGATGCAAGATGCTGCTGCTGCTGCTGCTGCTG 817
190 AsnValIleGlyThrGluAsp 196
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seq_name: qb_est1:A0124446

seq_documentation_block:

LOCUS A0124446 859 bp mRNA ESI 23-OCT-2000
DEFINITION A0124446 NT2RM4 Homo sapiens cDNA clone R12RM4000018 5', mRNA
sequence.

ACCESSION A0124446

VERSION A0124446.1 GI:10949162

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 859)

AUTHORS

Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J.,
Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
Isogai, T.
HRI human cDNA project (Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S.,
Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki,
Y., Sugano, S., Isogai, T.)

JOURNAL

Unpublished (2000)

COMMENT

Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yasa, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp

HRI human cDNA project; 5' & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction, Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. 859
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM4000018"
/clone_lib="NT2RM4"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/note="vector: pM18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"

FEATURES

SOURCE

BASE COUNT

ORIGIN

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Ratio: 5.378 Gaps: 1
Percent Similarity: 93.299 Percent Identity: 92.784

alignment_block:

us-09-525-998a-12 x A0124446

Align seg 1/1 to: A0124446 from: 1 to: 859


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106 sThrValAspArqAspThrValCysGlyCysArgLysAsnGlnThrArgH 123
|||||
541 CACAGCGACCGCGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 590
123 iStyTrpSerGluAsnLeuPheGlnCysPheAsnGlnCysSerLeuCysLeu 139
|||||
591 AATAAGCAGGAAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 156
|||||
641 AATGAGAGGCTGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 690
156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSer 172
|||||
691 CTGCAAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 740
173 AsnCysLysLysSerLeuGluCysThrLys 182
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741 AACTGCTGCAAAATGCGCAAAAGAAATGAGTCACAGTGGAGATCTCTCTTG 771

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DEFINITION 601448388F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852525 5',
mRNA sequence.
ACCESSION BE871809
VERSION BE871809.1 GI:10320585
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 969)
AUTHORS NIH-MGC http://mgc.nhl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D
Email: rcp@bbs-rnmail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/NIH-MGC at:
http://image.llnl.gov
plate: LAM9574 row: 6 column: 22
High quality sequence stop: 642.
location/Qualifiers
tag: 1..969
organism: "Homo sapiens"
db_xref="taxon:9606"
clone="IMAGE:3852525"
clone_lib="NIH_MGC_65"
library_type="adenocarcinoma"
lab_host="pBMT10 (phage-resistant)"
note="Single clone, Vector pCMV SV0016, Site 1, NotI,
Site 2, SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT 281 a 273 c 241 g 174 t
ORIGIN
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..
..
alignment_scores:
Quality: 94.00 Length: 165
Ratio: 5.671 Gaps: 1
Percent Similarity: 99.994 Percent Identity: 99.788
alignment_block:
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Align seq 1/1 to: BE871809 from: 1 to: 969

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53 ysglyThrTrpLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 69
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52 AAGCAACCTTACTTGTACAAATGACTGTCCAGCGCGCGCGCGCGCGCG 101
70 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuAr 86
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102 TGTAGGAGTGTGAGAGGAGGTCCTTCCATCCAGGCTTACAGAAACCA 151
86 gHisCysLeuSerCysSerLysCysArgLysGluMetGlyGlnValGlu 103
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152 ACACCTGCTTACGCTGTCTTAAATGCGGAAAGGAAATGGGCTTACGG 201
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120 GlnTrpArgHisTrpSerGluAsnLeuPheGlnCysPheAsnCysSe 136
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136 rLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGluLysGlnAsn 153
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170 SerCysSerAspCysLysLysSerLeuGluCysThrLysLeuCysLeu 186
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402 TGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 451
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DEFINITION AU125680 NT:39M4 Homo sapiens cDNA clone NT:PM4002005 5', mRNA
sequence.
ACCESSION AU125680
VERSION AU125680.1 GI:10950396
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS Ota,T., Wakamatsu,A., Oizawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project (Ota,T., Nakamatsu,A., Oizawa,M., Ishii,S.,
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
,Y., Sugano,S., Isogai,T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kasaragi, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5' & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of

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FEATURES
source
1. .817
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute,
Location/Qualifiers

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Percent Similarity: 91.713 Percent identity: 90.608
alignment_block:
US-09-525-998A-12 x A0125680
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17 MetLeuValGlyGlyGlyProSerGlyValGlyGly 29
324 GGTGTGGTGGGAAATATAGAGCTTAAAGGATATATGATGATGATGAT 373
30AspSerValCysProGlnGlyLysTyrlle 39
374 TAGGGACAGGACAGACAGACATAGTGTGTGCTCCCAAGCAAAATATATC 423
40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 56
424 CACGCTCAAAATATATGATGATGATGATGATGATGATGATGATGATG 473
56 MetLeuValAspCysProGlyProGlyGlnAspThrAspCysArgGlyC 73
474 CTGTACATACATGCTGTACAGGCTGGGGACAGATACGAGCTGAGGAGT 523
73 YsGlySerGlySerIleThrAlaSerGluAsnHisLeuArgHisCysLeu 89
524 GTCAGAGGGGCTGCTTACCGCTTACAGAAACACACACACACACACGTC 573
90 SerCysSerLysCysArgLysGlyMetGlyGlyValLeuLeuLeuSerCys 106
574 AGCTGTCTCAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 623
106 SerValAspArgAspThrValCysGlyCysArgCysAsnGlnIleTyArg 123
624 CACATGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 673
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674 ATATATGAGTCAAAAGGCTTTTACAGTCTTCAATATGAGGCTCTGCTC 723
140 AsnGlyThrValHisLeuSerCysGlnGlyGlyGlyGlyGlyGlyGly 156
724 ATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 773
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seq_name: ch_est2:B6677121
seq_documentation_block:

LOCUS B6677121 929 bp ssNA 101 MAY 2001
DEFINITION NT_004084.5 Homo sapiens cDNA clone IMAGE474614 5'.
mRNA sequence.
ACCESSION B6677121
VERSION B6677121.1 GI:13998518
KEYWORDS PSI.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 929)
AUTHORS NIH MCC helpdesk@mail.nih.gov
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: egapb@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIN at:
http://image.llnl.gov
Plasmid: L1AM10600 row: h column: 23
High fidelity sequence stop: 797.
Location/Qualifiers
1. 929
Organism="Homo sapiens"
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/tissue_type="squamous cell carcinoma"
/zinc_finger="ZnF1 (1 finger-resistant)"
/note="Organ: skin; Vector: pCMV-SpeK6; Size: 1. Not I.
Site 2: SalI; cloned unidirectionally. Primer: oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a MGC library."

FEATURES
source

alignment_scores:
Quality: 899.50 Length: 256
Ratio: 4.647 Caps: 8
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alignment_block:
US-09-525-998A-12 x B6677121
Align seq 1/1 to: B6677121 from: 1 to: 929

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200 CTATGGGAGATATATGATGATGATGATGATGATGATGATGATGATG 249
39 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThr 56
250 CACGCTCAAAATATATGATGATGATGATGATGATGATGATGATGATG 299
56 YsGlySerGlySerIleThrAlaSerGluAsnHisLeuArgHisCysLeu 72
300 ACTTGTACATACATGCTGTACAGGCTGGGGACAGATACGAGCTGAGG 349
73 CysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 89

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106  ystThrValAspArgAspThrValCysGlyCysArgGlyAsn.ClinlyrAr 122
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450  GCAATGTCAGACACACACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 499
122  qllstYrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysL 139
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139  euAsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCys 155
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550  TCAATGGACAGCTGACCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 599
156  thrCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSe 172
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600  ACCTGGATGGAGTTTCTTTCTAAGAGAGAAAGAGTGTGTGTGTGTGTGTAG 649
172  r..... 172
650  TAGACGCTCTGCTCTGCGGCGCAGCCCTTCGAAATGCACTGGCGGCGATCTCGG 699
172  ..... 172
700  GTCAATGCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 749
173  .....Asn.CysLysLysSerLeuGluCysThrLysL 183
   |||||
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183  eu.CysLeu.ProGlnIleGluAsnValLysGlyThrGluAspSer...G 198
   |||||
800  TGGTCCCTAACCCAGCAATTCAGACGTGTAAAGCCGCACTTCAGCGAGCTCAGG 849
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850  GTAGACACA 857
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